

SEQUENCE LISTING

<110> Gilbert, Teresa
 Hart, Charles E.
 Sheppard, Paul O.
 Gilbertson, Debra G.

<120> GROWTH FACTOR HOMOLOG ZVEGF4

<130> 99-19

<150> US 60/132,250

<151> 1999-05-03

<150> US 60/164,463

<151> 1999-11-10

<150> US 60/180,169

<151> 2000-02-04

<160> 53

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1882

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (226)...(1338)

<400> 1

```

ccgtcaccat ttatcagctc agcaccacaa ggaagtgcgg cacccacacg cgctcggaaa      60
gttcagcatg caggaagttt ggggagagct cggcgattag cacagcgacc cgggccagcg      120
cagggcgagc gcaggcgggc agagcgcagg gcggcgcggc gtcggtcccc ggagcagaac      180
ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg cac cgg ctc      237
                                         Met His Arg Leu

```

atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac	285
Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp	
5 10 15 20	
act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc	333
Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala	
25 30 35	
aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga	381
Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg	
40 45 50	
gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga	429
Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg	
55 60 65	
ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac	477
Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His	
70 75 80	
tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga	525
Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly	
85 90 95 100	
tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt	573
Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val	
105 110 115	
gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga	621
Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly	
120 125 130	
cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa	669
His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	
135 140 145	
atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag	717
Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys	
150 155 160	
att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag	765
Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu	
165 170 175 180	

acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac	813
Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn	
185 190 195	
tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa	861
Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys	
200 205 210	
aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat	909
Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn	
215 220 225	
cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct	957
Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro	
230 235 240	
cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg	1005
Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu	
245 250 255 260	
gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat	1053
Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn	
265 270 275	
tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc	1101
Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe	
280 285 290	
ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt	1149
Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys	
295 300 305	
gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg	1197
Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val	
310 315 320	
aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg	1245
Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg	
325 330 335 340	

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg aggggtgagat 1398
 aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
 agtgggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatataca 1518
 tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga gggtatatat 1578
 gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa tgtttttttt 1638
 ttttggtata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa 1698
 tcctttgcca aaataaggga tggtcгааata tatgaaacat gtcttttagaa aatttaggag 1758
 ataaatttat ttttaatttt tgaaacacga aacaattttg aatcttgctc tcttaaagaa 1818
 agcatcttgt atattaaaaa tcaaaagatg aggctttctt acatatacat cttagttgat 1878
 tatt 1882

<210> 2

<211> 370

<212> PRT

<213> Homo sapiens

<400> 2

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
 1 5 10 15
 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
 20 25 30
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
 85 90 95
 Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
 195 200 205
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 3

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide motif

<221> VARIANT

<222> (2)...(19)

<223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (20)...(34)
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT
 <222> (36)...(45)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (46)...(72)
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT
 <222> (74)...(93)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (94)...(123)
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT
 <222> (125)...(125)
 <223> Xaa = Any Amino Acid

<400> 3

Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10						15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30		
Xaa	Xaa	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40						45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55				60						
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75							80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90						95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105							110	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Cys			
			115					120					125			

<210> 4

<211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide motif

<221> VARIANT
 <222> (2)...(2)
 <223> Xaa = Lys or Arg

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa = Asp, Asn or Glu

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa = Trp, Tyr or Phe

<221> VARIANT
 <222> (6)...(16)
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> (17)...(20)
 <223> Xaa = Any Amino Acid or is not present

<221> VARIANT
 <222> (22)...(22)
 <223> Xaa = Lys or Arg

<221> VARIANT
 <222> (23)...(23)
 <223> Xaa = Trp, Tyr or Phe

<400> 4

Cys	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5					10					15	
Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Cys							
			20											

<210> 5
 <211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide tag

<400> 5
Glu Tyr Met Pro Met Glu
1 5

<210> 6
<211> 1110
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence

<221> misc_feature
<222> (1)...(1110)
<223> n = A,T,C or G

<400> 6

atgcaymgny	tnathttygt	ntayacnytn	athtgygcna	ayttytgyws	ntgymgngay	60
acnwsngcna	cncncarws	ngcnwsnath	aargcnytnm	gnaaygcnaa	yytnmgnmgn	120
gaygarwsna	aycayytnac	ngayytntay	mgnmnggayg	aracnathca	rgtnaarggn	180
aayggntayg	tncarwsncc	nmgnttyccn	aaywsntayc	cnmgnaayyt	nytnytnacn	240
tggmgnytn	aywsncarga	raayacnmgn	athcarytng	tnntygayaa	ycarttygg	300
ytnngargarg	cngaraayga	yathtgymgn	taygaytttg	tnngargtnga	rgayathwsn	360
garacnwsna	cnathathmg	nggnmgntgg	tgyggncaya	argargtncc	nccnmgnath	420
aarwsnmgna	cnaaycarat	haarathacn	ttyaarwsng	aygaytaytt	ygtngcnaar	480
ccnggnttya	arathtayta	ywsnytnytn	gargayttyc	arccngcngc	ngcnwsngar	540
acnaaytggg	arwsngtnac	nwsnwsnath	wsnggngtnw	sntayaayws	nccnwsngtn	600
acngayccna	cnytnathgc	ngaygcnytn	gayaaraara	thgcngartt	ygayacngtn	660
gargayytny	tnaartaytt	yaayccngar	wsntggcarg	argayytnga	raayatgtay	720
ytngayacnc	cnmgntaymg	nggnmgnwsn	taycaygaym	gnaarwsnaa	rgtngayytn	780
gaymgnytna	aygaygaygc	naarmgntay	wsntgyacnc	cnmgnaayta	ywsngtnaay	840
athmgngarg	arytnaaryt	ngcnaaygtn	gtnttyttyc	cnmgntgyyt	nytngtncar	900
mgntgyggng	gnaaytgygg	ntgyggnacn	gtnaaytggm	gnwsntgyac	ntgyaaywsn	960
ggnaaracng	tnaaraarta	ycaygargtn	ytncarttyg	arccnggnca	yathaarmgn	1020
mgnggnmgng	cnaaracnat	ggcnytnngtn	gayathcary	tngaycayca	ygarmgntgy	1080
gaytgyatht	gywsnwsnmg	nccnccnmgn				1110

<210> 7
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 7
 mgntgyggng gnaaytg

17

<210> 8
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 8
 mgntgydsng gnwrytg

17

<210> 9
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 9

carywnccns hrcanck

17

<210> 10
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 10
 ttyttyccnm gntgyyt

17

<210> 11
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 11
 ntnddnccnn sntgybt

17

<210> 12
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide primer

 <221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 12
avrcansng gnhhnan 17

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(17)
<223> n = A,T,C or G

<400> 13
caygarmgnt gygaytg 17

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature
<222> (1)...(17)
<223> n = A,T,C or G

<400> 14
caynnnnvnt gyvvntg 17

<210> 15
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(17)
 <223> n = A,T,C or G

<400> 15
 canbbrcanb nnnnrtg

17

<210> 16
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 16
 tgyacnccnm gnaayta

17

<210> 17
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 17
 tgyhnnmcnm knrmndh

17

<210> 18
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 18
 dhnkynmkng knndrca

17

<210> 19
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(18)
 <223> n = A,T,C or G

<400> 19
 ntaygaytwy gtngargt

18

<210> 20
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer

<221> misc_feature
 <222> (1)...(18)
 <223> n = A,T,C or G

<400> 20
 natrcdrawr canctyca

18

<210> 21
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<223> oligonucleotide primer

<221> misc feature

$\langle 222 \rangle$ (1) ... (18)

<223> n = A, T, C. or G

gntdbccnma ndvntayc.

18

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

<223> oligonucleotide primer

<221> misc feature

 $\langle 222 \rangle \quad (1) \dots (18)$

<223> n = A, T, C or G

cnahvggnkt nhbnatrg

18

<210> 23

<211> 18

<212> DNA

<213> Artificial Sequence

<223> oligonucleotide primer

<221> misc feature.

<222> (1)...(18)

<223> n = A, T, C or G

tnhdnggnmr ntdbtgyg

18

.<210> 24

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer

<221> misc_feature

<222> (1)...(18)

<223> n = A,T,C or G

<400> 24

andhnccnky nahvacrc

18

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21,119

<400> 25

aggacgatgg tgtggacaca agga

24

<210> 26

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21,120

<400> 26

tccagagcat ccgcaatcag agtg

24

<210> 27

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21,987

<400> 27

caacctgttg tttgtcccgt cacc

24

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17.251

<400> 28

tctggacgtc ctctgctgg tatag

25

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17.252

<400> 29

ggtatggagc aaggggcaag ttggg

25

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17.156

<400> 30

gagtggcaac ttccagggcc aggagag

27

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC17.157

<400> 31
cttttgctag cctcaaccct gactatc

27

<210> 32
<211> 1760
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (154)...(1191)

<400> 32
attatgtgga aactaccctg cgattctctg ctgccagagc aggctcggcg cttccacccc 60
agtgcagcct tcccctggcg gtggtgaaag agactcggga gtcgctgctt ccaaagtgcc 120
cgccgtgagt gagctctcac cccagtcagc caa atg agc ctc ttc ggg ctt ctc 174
Met Ser Leu Phe Gly Leu Leu
1 5
ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa 222
Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu
10 15 20
tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac 270
Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn
25 30 35
gga gta caa gat cct cag cat gag aga att att act gtg tct act aat 318
Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn
40 45 50 55
gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg 366
Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr
60 65 70
gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa 414
Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln
75 80 85
ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata 462
Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile
90 95 100

tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata	510
Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile	
105 110 115	
tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct	558
Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser	
120 125 130 135	
aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct	606
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro	
140 145 150	
tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc	654
Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe	
155 160 165	
aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg	702
Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu	
170 175 180	
gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt	750
Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu	
185 190 195	
att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta	798
Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu	
200 205 210 215	
tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga	846
Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg	
220 225 230	
aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta	894
Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu	
235 240 245	
tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta	942
Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu	
250 255 260	
aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc	990
Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg	
265 270 275	

Met Ser Leu Phe Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
1 5 10 15
Arg Gln Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
20 25 30
Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
35 40 45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
 50 55 60
 His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
 65 70 75 80
 Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
 85 90 95
 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
 100 105 110
 Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
 115 120 125
 Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
 130 135 140
 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
 145 150 155 160
 Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
 165 170 175
 Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
 180 185 190
 Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
 195 200 205
 Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
 210 215 220
 Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
 225 230 235 240
 Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
 245 250 255
 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
 260 265 270
 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
 275 280 285
 His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
 290 295 300
 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
 305 310 315 320
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
 325 330 335
 Cys Val Cys Arg Gly Ser Thr Gly Gly
 340 345

<210> 34

<211> 3571

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1049)...(2086)

<400> 34

```

gaattcccgg gtcgaccac gcgtccgggc gccagggga aaggaagctg ggggccgcct 60
ggcggcattc ctgcccagc tgtgggctcc gtctgcccg gggcccgcag tgccccctgt 120
ctgcgccagc acctgttggc ccgccagctg gccgcccgcg cccccgcgc cccccgcgcc 180
cgcccgggcg ccagccccgc gcccgcgcg ccgcccgcgt ggggaaagtg gagacgggga 240
ggggacaaga gcgatcctcc aggccagcca ggccttccct tagccgcccg tgcttagccg 300
ccacctctcc tcagccctgc gtctgccct gccttagggc aggcattccga gcgctcgcga 360
ctccgagccg cccaagctct cccggcttcc cgcagcactt cgccggtacc cgagggaact 420
tcggtggcca ccgactgcag caaggaggag gctccgcggt ggatccgggc cagtcccag 480
tcgtccccgc ggcctctctg cccgcccggg acccgcgcg cactcgcagg gcacggtccc 540
ctccccccag gtgggggtgg ggcgccgcct gccgcccga tcagcagctt tgcattgat 600
cccaaggtag tcgctcgtc gccgacctg cttccagtct ggcttggcgg gaccccagat 660
cctcgctgtg gtctgtccc ccaaactgac aggtgctccc tgcgagtcgc cacgactcat 720
cgccgtccc ccgctcccc accccttctt tcctccctc cctaccccca cccccgcac 780
ttcggcacag ctcaggattt gtttaaacct tgggaaactg gttcagggtc aggttttgc 840
ttgatccttt tcaaaaactg gagacacaga agagggtctt aggaaaaact tttggatggg 900
attatgtgga aactaccctg cgattctctg ctgccagagc cggccaggcg cttccaccgc 960
agcgcagcct ttccccggct gggctgagcc ttggagtcgt cgcttcccca gtgcccgcg 1020
cgagttagcc ctgccccag tcagccaa atg ctc ctc ctc ggc ctc ctc ctg 1072

```

Met Leu Leu Leu Gly Leu Leu Leu

1

5

```

ctg aca tct gcc ctg gcc ggc caa aga acg ggg act cgg gct gag tcc 1120
Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser

```

10

15

20

```

aac ctg agc agc aag ttg cag ctc tcc agc gac aag gaa cag aac gga 1168
Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly

```

25

30

35

40

```

gtg caa gat ccc cgg cat gag aga gtt gtc act ata tct ggt aat ggg 1216
Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly

```

45

50

55

```

agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg 1264
Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val

```

60

65

70

ctg	gtg	tgg	aga	tta	gtt	gca	gta	gat	gaa	aat	gtg	cgg	atc	cag	ctg	1312
Leu	Val	Trp	Arg	Leu	Val	Ala	Val	Asp	Glu	Asn	Val	Arg	Ile	Gln	Leu	
		75					80					85				
aca	ttt	gat	gag	aga	ttt	ggg	ctg	gaa	gat	cca	gaa	gac	gat	ata	tgc	1360
Thr	Phe	Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	
	90					95					100					
aag	tat	gat	ttt	gta	gaa	gtt	gag	gag	ccc	agt	gat	gga	agt	gtt	tta	1408
Lys	Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Ser	Val	Leu	
105					110					115					120	
gga	cgc	tgg	tgt	ggt	tct	ggg	act	gtg	cca	gga	aag	cag	act	tct	aaa	1456
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Thr	Ser	Lys	
				125					130					135		
gga	aat	cat	atc	agg	ata	aga	ttt	gta	tct	gat	gag	tat	ttt	cca	tct	1504
Gly	Asn	His	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	Pro	Ser	
			140					145					150			
gaa	ccc	gga	ttc	tgc	atc	cac	tac	agt	att	atc	atg	cca	caa	gtc	aca	1552
Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Ser	Ile	Ile	Met	Pro	Gln	Val	Thr	
		155					160					165				
gaa	acc	acg	agt	cct	tcg	gtg	ttg	ccc	cct	tca	tct	ttg	tca	ttg	gac	1600
Glu	Thr	Thr	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ser	Leu	Ser	Leu	Asp	
	170					175					180					
ctg	ctc	aac	aat	gct	gtg	act	gcc	ttc	agt	acc	ttg	gaa	gag	ctg	att	1648
Leu	Leu	Asn	Asn	Ala	Val	Thr	Ala	Phe	Ser	Thr	Leu	Glu	Glu	Leu	Ile	
185					190					195					200	
cgg	tac	cta	gag	cca	gat	cga	tgg	cag	gtg	gac	ttg	gac	agc	ctc	tac	1696
Arg	Tyr	Leu	Glu	Pro	Asp	Arg	Trp	Gln	Val	Asp	Leu	Asp	Ser	Leu	Tyr	
				205					210					215		
aag	cca	aca	tgg	cag	ctt	ttg	ggc	aag	gct	ttc	ctg	tat	ggg	aaa	aaa	1744
Lys	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	Ala	Phe	Leu	Tyr	Gly	Lys	Lys	
			220					225					230			
agc	aaa	gtg	gtg	aat	ctg	aat	ctc	ctc	aag	gaa	gag	gta	aaa	ctc	tac	1792
Ser	Lys	Val	Val	Asn	Leu	Asn	Leu	Leu	Lys	Glu	Glu	Val	Lys	Leu	Tyr	
		235					240					245				

agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag 1840
 Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys
 250 255 260

agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt 1888
 Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys
 265 270 275 280

gga gga aat tgt gcc tgt tgt ctc cat aat tgc aat gaa tgt cag tgt 1936
 Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys
 285 290 295

gtc cca cgt aaa gtt aca aaa aag tac cat gag gtc ctt cag ttg aga 1984
 Val Pro Arg Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg
 300 305 310

cca aaa act gga gtc aag gga ttg cat aag tca ctc act gat gtg gct 2032
 Pro Lys Thr Gly Val Lys Gly Leu His Lys Ser Leu Thr Asp Val Ala
 315 320 325

ctg gaa cac cac gag gaa tgt gac tgt gtg tgt aga gga aac gca gga 2080
 Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Asn Ala Gly
 330 335 340

ggg taa ctgcagcctt cgtagcagca cacgtgagca ctggcattct gtgtaccccc 2136
 Gly *
 345

acaagcaacc ttcatcccca ccagcgttgg ccgcagggct ctcagctgct gatgctggct 2196
 atggtaaaga tcttactcgt ctccaaccaa attctcagtt gtttgcttca atagccttcc 2256
 cctgcaggac ttcaagtgtc ttctaaaaga ccagaggcac caagaggagt caatcacaaa 2316
 gcaactgcctt ctgaggaag ccagacaat ggtcttctga ccacagaaac aaatgaaatg 2376
 aatgtagatc gctagcaaac tctggagtga cagcatttct tttccactga cagaatgggt 2436
 tagcttagtt gtcttgatat gggcaagtga tgtcagcaca agaaaatggt gaaaaacaca 2496
 cacttgattg tgaacaatgc agaaatactt ggatttctcc aacctgtttg catagataga 2556
 cagatgctct gttttctaca aactcaaagc ttttagagag cagctatggt aataggaatt 2616
 aaatgtgcca tgctgaaagg aaagactgaa gttttcaatg cttggcaact tctccgcaat 2676
 ttggaggaaa ggtgcggtca tggtttgagg aaagcacacc tgcacagagg agtggccttc 2736
 ccttcccttc cctctgaggt ggcttctgtg tttcattgtg tatattttta tattctcctt 2796
 ttgacattat aactgttggc ttttctaata ttgttaaata tttctatttt taccaaaggt 2856
 atttaatatatt cttttttatg acaacctaga gcaattattt ttagcttgat aatttttttt 2916
 tctaaacaaa attgttatag ccagaagaac aaagatgatt gatataaaaa tcttgttgct 2976

ctgacaaaaa catatgtatt tcttccttgt atggtgctag agcttagcgt catctgcatt 3036
 tgaaaagatg gaatggggaa gtttttagaa ttggtaggtc gcagggacag tttgataaca 3096
 actgtactat catcaattcc caattctgtt cttagagcta cgaacagaac agagcttgag 3156
 taaatatgga gccattgcta acctaccctt ttctatggga aataggagta tagctcagag 3216
 aagcacgtcc ccagaaacct cgaccatttc taggcacagt gttctgggct atgctgcgct 3276
 gtatggacat atcctattta tttcaatact agggttttat tacctttaaa ctctgctcca 3336
 tacacttgta ttaatacatg gatattttta tgtacagaag tatatcattt aaggagtcca 3396
 cttattatac tctttggcaa ttgcaaagaa aatcaacata atacattgct tgtaaagtct 3456
 taatctgtgc ccaagttttg tggtgactat ttgaattaaa atgtattgaa tcatcaaata 3516
 aaataatctg gctatttttg ggaaaaaaaa aaaaaaaaaa aaaaagggcg gccgc 3571

<210> 35

<211> 345

<212> PRT

<213> Mus musculus

<400> 35

Met Leu Leu Leu Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
 1 5 10 15
 Arg Thr Gly Thr Arg Ala Glu Ser Asn Leu Ser Ser Lys Leu Gln Leu
 20 25 30
 Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
 35 40 45
 Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
 50 55 60
 His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
 65 70 75 80
 Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
 85 90 95
 Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
 100 105 110
 Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
 115 120 125
 Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
 130 135 140
 Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
 145 150 155 160
 Ser Ile Ile Met Pro Gln Val Thr Glu Thr Thr Ser Pro Ser Val Leu
 165 170 175
 Pro Pro Ser Ser Leu Ser Leu Asp Leu Leu Asn Asn Ala Val Thr Ala
 180 185 190
 Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
 195 200 205

Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
 210 215 220
 Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu
 225 230 235 240
 Leu Lys Glu Glu Val Lys Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
 245 250 255
 Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
 260 265 270
 Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
 275 280 285
 His Asn Cys Asn Glu Cys Gln Cys Val Pro Arg Lys Val Thr Lys Lys
 290 295 300
 Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu
 305 310 315 320
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
 325 330 335
 Cys Val Cys Arg Gly Asn Ala Gly Gly
 340 345

<210> 36
 <211> 600
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (496)...(592)

<400> 36

gtgggaagag	tcccgccgg	cgattaaact	gggcatgctc	agtggcagag	caggtttagg	60
cccggcctgg	gaaactgggg	agctgaggtg	ctcgccgcgc	cgctctgagc	ccgagtgcgc	120
gcctctcagg	ggccgcggcc	ggggctggag	aacgctgctg	ctccgctcgc	ctgccccgct	180
agattcggcg	ctgcccggcc	cctgcagcct	gtgctgcagc	tgccggccac	cggagggggc	240
gaacaaacaa	acgtcaacct	gttgtttgtc	ccgtcaccat	ttatcagctc	agcaccacaa	300
ggaagtgcgg	caccacacag	cgctcggaaa	gttcagcatg	caggaagttt	ggggagagct	360
cggcgattag	cacagcgacc	cgggccagcg	cagggcgagc	gcagacggcg	agagcgcagg	420
gcggcgcggc	gtcgggtccc	ggagcagaac	ccggcttttt	cttgagcgca	cgctgtctct	480
agtcgctgat	cccaa atg	cac cgg ctc	atc ttt gtc	tac act cta	atc tgc	531
	Met	His	Arg	Leu	Ile Phe Val Tyr Thr Leu Ile Cys	
	1		5		10	

gca aac ttt tgc agc tgt cgg gac act tct gca acc ccg cag agc gca 579
 Ala Asn Phe Cys Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala
 15 20 25

tcc atc aaa gct t gagtattc 600
 Ser Ile Lys Ala
 30

<210> 37
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC22,685

<400> 37
 gccgtcacca tttatcag 18

<210> 38
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC22,686

<400> 38
 cgggtcgctg tgctaadc 18

<210> 39
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide

<400> 39
 Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln
 1 5 10 15
 Ile Lys

<210> 40
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide

<400> 40
 Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg
 1 5 10 15
 Tyr Arg Gly Arg Ser Tyr His Asp Cys
 20 25

<210> 41
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide

<400> 41
 Cys Phe Glu Pro Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met
 1 5 10 15
 Ala Leu Val Asp Ile Gln Leu Asp
 20

<210> 42
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide

<400> 42
 Glu Tyr Met Pro Thr Asp
 1 5

<210> 43

ccacttggtg tcatgcat gca

23

<210> 47
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC27116

<400> 47
 attataggat ccgagtatat gcctatggag gttgacctgg ataggctcaa tgatgatgcc 60

<210> 48
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC26137

<400> 48
 attatatggc gcgccttatc gaggtggtct tgagct 36

<210> 49
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC26317

<400> 49
 atcacctcac agacttgtag cagag 25

<210> 50
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC26318

<400> 50
 cctacaaatg tcattttctg cttcc 25

<210> 51
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC14063

<400> 51
 caccagacat aatagctgac agact 25

<210> 52
 <211> 1472
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (93)...(1205)

<400> 52
 agggactgtg cagtagaaat cgcgcgactc aaccctttgg gctttattta tttacttttg 60
 gagcaacgcg atccctaggt cgctgagccc aa atg caa cgg ctc gtt tta gtc 113
 Met Gln Arg Leu Val Leu Val
 1 5

tcc att ctc ctg tgc gcg aac ttt agc tgc tat ccg gac act ttt gcg 161
 Ser Ile Leu Leu Cys Ala Asn Phe Ser Cys Tyr Pro Asp Thr Phe Ala
 10 15 20

act ccg cag aga gca tcc atc aaa gct ttg cgc aat gcc aac ctc agg 209
 Thr Pro Gln Arg Ala Ser Ile Lys Ala Leu Arg Asn Ala Asn Leu Arg
 25 30 35

aga gat gag agc aat cac ctc aca gac ttg tac cag aga gag gag aac 257
 Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Gln Arg Glu Glu Asn
 40 45 50 55

att cag gtg aca agc aat ggc cat gtg cag agt cct cgc ttc ccg aac 305
 Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro Asn
 60 65 70

agc	tac	cca	agg	aac	ctg	ctt	ctg	aca	tgg	tgg	ctc	cgt	tcc	cag	gag	353
Ser	Tyr	Pro	Arg	Asn	Leu	Leu	Leu	Thr	Trp	Trp	Leu	Arg	Ser	Gln	Glu	
			75					80					85			
aaa	aca	cgg	ata	caa	ctg	tcc	ttt	gac	cat	caa	ttc	gga	cta	gag	gaa	401
Lys	Thr	Arg	Ile	Gln	Leu	Ser	Phe	Asp	His	Gln	Phe	Gly	Leu	Glu	Glu	
		90					95					100				
gca	gaa	aat	gac	att	tgt	agg	tat	gac	ttt	gtg	gaa	gtt	gaa	gaa	gtc	449
Ala	Glu	Asn	Asp	Ile	Cys	Arg	Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Val	
	105					110					115					
tca	gag	agc	agc	act	gtt	gtc	aga	gga	aga	tgg	tgt	ggc	cac	aag	gag	497
Ser	Glu	Ser	Ser	Thr	Val	Val	Arg	Gly	Arg	Trp	Cys	Gly	His	Lys	Glu	
120					125					130					135	
atc	cct	cca	agg	ata	acg	tca	aga	aca	aac	cag	att	aaa	atc	aca	ttt	545
Ile	Pro	Pro	Arg	Ile	Thr	Ser	Arg	Thr	Asn	Gln	Ile	Lys	Ile	Thr	Phe	
				140					145					150		
aag	tct	gat	gac	tac	ttt	gtg	gca	aaa	cct	gga	ttc	aag	att	tat	tat	593
Lys	Ser	Asp	Asp	Tyr	Phe	Val	Ala	Lys	Pro	Gly	Phe	Lys	Ile	Tyr	Tyr	
			155					160					165			
tca	ttt	gtg	gaa	gat	ttc	caa	ccg	gaa	gca	gcc	tca	gag	acc	aac	tgg	641
Ser	Phe	Val	Glu	Asp	Phe	Gln	Pro	Glu	Ala	Ala	Ser	Glu	Thr	Asn	Trp	
		170					175					180				
gaa	tca	gtc	aca	agc	tct	ttc	tct	ggg	gtg	tcc	tat	cac	tct	cca	tca	689
Glu	Ser	Val	Thr	Ser	Ser	Phe	Ser	Gly	Val	Ser	Tyr	His	Ser	Pro	Ser	
	185					190					195					
ata	acg	gac	ccc	act	ctc	act	gct	gat	gcc	ctg	gac	aaa	act	gtc	gca	737
Ile	Thr	Asp	Pro	Thr	Leu	Thr	Ala	Asp	Ala	Leu	Asp	Lys	Thr	Val	Ala	
200					205					210					215	
gaa	ttc	gat	acc	gtg	gaa	gat	cta	ctt	aag	cac	ttc	aat	cca	gtg	tct	785
Glu	Phe	Asp	Thr	Val	Glu	Asp	Leu	Leu	Lys	His	Phe	Asn	Pro	Val	Ser	
				220					225					230		
tgg	caa	gat	gat	ctg	gag	aat	ttg	tat	ctg	gac	acc	cct	cat	tat	aga	833
Trp	Gln	Asp	Asp	Leu	Glu	Asn	Leu	Tyr	Leu	Asp	Thr	Pro	His	Tyr	Arg	
			235					240					245			

ggc agg tca tac cat gat cgg aag tcc aaa gtg gac ctg gac agg ctc 881
 Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu
 250 255 260

aat gat gat gtc aag cgt tac agt tgc act ccc agg aat cac tct gtg 929
 Asn Asp Asp Val Lys Arg Tyr Ser Cys Thr Pro Arg Asn His Ser Val
 265 270 275

aac ctc agg gag gag ctg aag ctg acc aat gca gtc ttc ttc cca cga 977
 Asn Leu Arg Glu Glu Leu Lys Leu Thr Asn Ala Val Phe Phe Pro Arg
 280 285 290 295

tgc ctc ctc gtg cag cgc tgt ggt ggc aac tgt ggt tgc gga act gtc 1025
 Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys Gly Thr Val
 300 305 310

aac tgg aag tcc tgc aca tgc agc tca ggg aag aca gtg aag aag tat 1073
 Asn Trp Lys Ser Cys Thr Cys Ser Ser Gly Lys Thr Val Lys Lys Tyr
 315 320 325

cat gag gta ttg aag ttt gag cct gga cat ttc aag aga agg ggc aaa 1121
 His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly Lys
 330 335 340

gct aag aat atg gct ctt gtt gat atc cag ctg gat cat cat gag cga 1169
 Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu Arg
 345 350 355

tgt gac tgt atc tgc agc tca aga cca cct cga taa aacactatgc 1215
 Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

acatctgtac ttgattatg aaaggacctt taggttacaa aaaccctaag aagcttctaa 1275
 tctcagtgc atgaatgcat atggaaatgt tgctttgtta gtgccatggc aagaagaagc 1335
 aaatatcatt aatttctata tacataaaca taggaattca cttatcaata gtatgtgaag 1395
 atatgtatat atacttatat acatgactag ctctatgtat gtaaatagat taaatacttt 1455
 attcagtata ttactg 1472

<210> 53

<211> 370

<212> PRT

<213> Mus musculus

Met	Gln	Arg	Leu	Val	Leu	Val	Ser	Ile	Leu	Leu	Cys	Ala	Asn	Phe	Ser
1				5				10					15		
Cys	Tyr	Pro	Asp	Thr	Phe	Ala	Thr	Pro	Gln	Arg	Ala	Ser	Ile	Lys	Ala
			20					25					30		
Leu	Arg	Asn	Ala	Asn	Leu	Arg	Arg	Asp	Glu	Ser	Asn	His	Leu	Thr	Asp
		35					40					45			
Leu	Tyr	Gln	Arg	Glu	Glu	Asn	Ile	Gln	Val	Thr	Ser	Asn	Gly	His	Val
	50					55					60				
Gln	Ser	Pro	Arg	Phe	Pro	Asn	Ser	Tyr	Pro	Arg	Asn	Leu	Leu	Leu	Thr
65					70					75					80
Trp	Trp	Leu	Arg	Ser	Gln	Glu	Lys	Thr	Arg	Ile	Gln	Leu	Ser	Phe	Asp
			85						90					95	
His	Gln	Phe	Gly	Leu	Glu	Glu	Ala	Glu	Asn	Asp	Ile	Cys	Arg	Tyr	Asp
			100					105					110		
Phe	Val	Glu	Val	Glu	Glu	Val	Ser	Glu	Ser	Ser	Thr	Val	Val	Arg	Gly
		115					120					125			
Arg	Trp	Cys	Gly	His	Lys	Glu	Ile	Pro	Pro	Arg	Ile	Thr	Ser	Arg	Thr
	130					135					140				
Asn	Gln	Ile	Lys	Ile	Thr	Phe	Lys	Ser	Asp	Asp	Tyr	Phe	Val	Ala	Lys
145					150					155					160
Pro	Gly	Phe	Lys	Ile	Tyr	Tyr	Ser	Phe	Val	Glu	Asp	Phe	Gln	Pro	Glu
			165						170					175	
Ala	Ala	Ser	Glu	Thr	Asn	Trp	Glu	Ser	Val	Thr	Ser	Ser	Phe	Ser	Gly
			180					185					190		
Val	Ser	Tyr	His	Ser	Pro	Ser	Ile	Thr	Asp	Pro	Thr	Leu	Thr	Ala	Asp
		195					200					205			
Ala	Leu	Asp	Lys	Thr	Val	Ala	Glu	Phe	Asp	Thr	Val	Glu	Asp	Leu	Leu
	210					215					220				
Lys	His	Phe	Asn	Pro	Val	Ser	Trp	Gln	Asp	Asp	Leu	Glu	Asn	Leu	Tyr
225					230					235					240
Leu	Asp	Thr	Pro	His	Tyr	Arg	Gly	Arg	Ser	Tyr	His	Asp	Arg	Lys	Ser
			245						250					255	
Lys	Val	Asp	Leu	Asp	Arg	Leu	Asn	Asp	Asp	Val	Lys	Arg	Tyr	Ser	Cys
		260						265					270		
Thr	Pro	Arg	Asn	His	Ser	Val	Asn	Leu	Arg	Glu	Glu	Leu	Lys	Leu	Thr
		275					280					285			
Asn	Ala	Val	Phe	Phe	Pro	Arg	Cys	Leu	Leu	Val	Gln	Arg	Cys	Gly	Gly
	290					295					300				
Asn	Cys	Gly	Cys	Gly	Thr	Val	Asn	Trp	Lys	Ser	Cys	Thr	Cys	Ser	Ser
305					310						315				320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly
325 330 335
His Phe Lys Arg Arg Gly Lys Ala Lys Asn Met Ala Leu Val Asp Ile
340 345 350
Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
355 360 365
Pro Arg
370

[illegible]